

09/508418

514 Rec'd PCT/PCT 13 MAR 2000

[Sequence Listing]

SEQ ID No: 1

Length of Sequence: 1874

5

Type of Sequence: Nucleic Acid

Topology: Linear

Strandness: Double strands

Kinds of Sequence: cDNA to mRNA

Origin

10

Organism Name: Tobacco (*Nicotiana tabacum*)

Strain name: Xanthi NC

Character of Sequence

Sign designating character: CDS

Position that locates: 26..1672

15

Way of determining character: P

AGCGCGGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT 52

Met Thr Thr Thr Pro Ile Ala Asn His

20

1 5

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA 100

Pro Asn Ile Phe Thr His Gln Ser Ser Ser Pro Leu Ala Phe Leu

10 15 20 25

25

AAC CGT ACG ACT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT 148

Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser

30 35 40

	GTC AAT TGC AAT GGC TGG AGA ACA CGA TCC TCC GTT GCC AAA GAT TAC		196	
	Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr			
	45	50	55	
5	ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC		244	
	Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp			
	60	65	70	
10	TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG		292	
	Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val			
	75	80	85	
15	ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT		340	
	Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg			
	90	95	100	105
20	GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA		388	
	Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu			
	110	115	120	
25	GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA		436	
	Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala			
	125	130	135	
	GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG		484	
	Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala			
	140	145	150	
	CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA		532	

Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys

155 160 165

CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG 580

5 Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu

170 175 180 185

AGA GCT GGT TTT GGT GCC ATT GGC CTC CGC CCT TCA CCT CCA GGT CAT 628

Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His

10 190 195 200

GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GGC GAA GTC 676

Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val

205 210 215

15 TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GCT GGT GAT 724

Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp

220 225 230

20 CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG 772

Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu

235 240 245

GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG 820

25 Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys

250 255 260 265

GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA 868

Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys

	270	275	280	
	CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG			916
	Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu			
	285	290	295	
5				
	CCG GAT GCA ATC AGT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG			964
	Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp			
	300	305	310	
10	AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA			1012
	Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr			
	315	320	325	
	TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC			1060
15	Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val			
	330	335	340	345
	ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG			1108
	Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser			
20	350	355	360	
	GTT GCC GCA GCA GAT GCA CTT TCA ATT TTC TAC TAT CCC CCA GTT GGA			1156
	Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly			
	365	370	375	
25	GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG			1204
	Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu			
	380	385	390	

	GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG		1252
	Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln		
395	400	405	
5	CGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC		1300
	Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn		
410	415	420	425
10	CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA		1348
	Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala		
	430	435	440
15	AAA AAT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA		1396
	Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val		
	445	450	455
20	GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT		1444
	Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp		
	460	465	470
25	CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT		1492
	Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe		
	475	480	485
	TTG GTT GGT CAT CTG GAT ACG CTA AGT ACT GCA AAA GCT GCT ATG AAT		1540
	Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn		
	490	495	500
	GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT AAT TAT GTG TCA GGT		1588

Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly

510

515

520

GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG 1636

5 Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu

525

530

535

GTA ACA CGA TTT CTG TCT CCG TAT GCA TAC AAA TGAAACCTGT GTTGGGGTA 1689

Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys

10

540

545

GTCCAACCT TGTTAGTAGT ACGATCATGC CTTGGGAAA TTGGCATGTG CCTAAAAGTT 1749

TTGCTCATTA GAGTTATTTT AGCCTTGGTA AATGATTGT ACTTGATATC AGTCGTTTC 1809

TTTGAGATAA AATGTTCTG TTCAGGAAT AATATGTATA TCAATTTAA ACAAAAAAAA 1869

AAAAA 1874

15

SEQ ID No.: 2

Length of Sequence: 548

Type of Sequence: Amino acid

Topology: Linear

5 Kind of Sequence: Protein

Origin:

Organism Name: Tobacco (*Nicotiana tabacum*)

Strain name: SR1

10

Met Thr Thr Thr Pro Ile Ala Asn His Pro Asn Ile Phe Thr His Gln
1 5 10 15

Ser Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro
15 20 25 30

Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg
35 40 45

20 Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val
50 55 60

Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly
65 70 75 80

25 Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn
85 90 95

Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr

100 105 110

Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln

115 120 125

5

Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp

130 135 140

Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys

10 145 150 155 160

Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe

165 170 175

15 Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Ala Ile

180 185 190

Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe

195 200 205

20

Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro

210 215 220

Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys

25 225 230 235 240

Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile

245 250 255

Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys

260 265 270

Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Gly Gln Thr Val Gly

5 275 280 285

Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg

290 295 300

10 Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys

305 310 315 320

Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val

325 330 335

15

Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val

340 345 350

Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu

20 355 360 365

Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro

370 375 380

25 Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly

385 390 395 400

Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr

405 410 415

Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val

420 425 430

5 Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser

435 440 445

Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys

450 455 460

10

Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg

465 470 475 480

Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr

15 485 490 495

Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu

500 505 510

20 Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val

515 520 525

Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg

530 535 540

25

Tyr Ala Tyr Lys

545

SEQ ID No.: 3

Length of Sequence: 1874

type of Sequence: Nucleic acid

Topology: Linear

5 Strandness: Double strands

Kind of Sequence: cDNA to mRNA

Origin

Organism Name: tobacco (Nicotiana tabacum)

Strain Name: SRI

10 Character of Sequence

Signal designating Character: CDS

Location: 26..1672

way for determining Character: P

15

AGCGCCGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT	52
Met Thr Thr Pro Ile Ala Asn His	

1	5
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20

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA	100
Pro Asn Ile Phe Thr His Gln Ser Ser Ser Pro Leu Ala Phe Leu	

10	15	20	25
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25 AAC CGT ACG AGT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT	148
Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser	

30	35	40
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GTC AAT TGC AAT GGC TGG AGA ACA CGA TGC TCC GTT GCC AAA GAT TAC 196

	Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr			
	45	50	55	
	ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC			244
5	Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp			
	60	65	70	
	TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG			292
	Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val			
10	75	80	85	
	ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT			340
	Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg			
	90	95	100	105
15				
	GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA			388
	Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu			
	110	115	120	
20	GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA			436
	Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala			
	125	130	135	
	GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG			484
25	Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala			
	140	145	150	
	CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA			532
	Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys			

	155	160	165	
	CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG			580
	Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu			
5	170	175	180	185
	AGA GCT GGT TTT GGT GCC ATT GCC CTC CGC CCT TCA CCT CCA GGT CAT			628
	Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His			
	190	195	200	
10				
	GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GCC GAA GTC			676
	Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val			
	205	210	215	
15				
	TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GTT GGT GAT			724
	Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Val Gly Asp			
	220	225	230	
20				
	CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG			772
	Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu			
	235	240	245	
25				
	GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG			820
	Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys			
	250	255	260	265
30				
	GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA			868
	Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys			
	270	275	280	

	CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG	916		
	Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu			
	285	290	295	
5	CCG GAT GCA ATC ACT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG	964		
	Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp			
	300	305	310	
	AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA	1012		
10	Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr			
	315	320	325	
	TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC	1060		
	Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val			
15	330	335	340	345
	ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG	1108		
	Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser			
	350	355	360	
20	GTT GCC GCA GCA GAT GCA CTT TCA AAT TTC TAC TAT CCC CCA GTT GGA	1156		
	Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly			
	365	370	375	
25	GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG	1204		
	Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu			
	380	385	390	
	GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG	1252		

	Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln		
395	400	405	
	GGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC		1300
5	Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn		
410	415	420	425
	CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA		1348
	Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala		
10	430	435	440
	AAA ATT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA		1396
	Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val		
15	445	450	455
	GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT		1444
	Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp		
	460	465	470
20	CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT		1492
	Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe		
	475	480	485
	TTG GTT GGT CAT CTG GAT ACG CTA ACT GCA AAA GCT GCT ATG AAT		1540
25	Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn		
	490	495	500
	GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT ATT TAT GTG TCA GGT		1588
	Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly		

510

515

520

GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG 1636

Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu

5

525

530

535

GTA ACA GGA TTT CTG TCT CGG TAT GCA TAC AAA TGAAACCTGT GTTGGGGTA 1689

Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys

540

545

10 GTCCAAGACCT TGTTAGTAGT ACGATCATGCC CTTGGGAAAA TTGGCATGTG CCTAAAAGTT 1749

TTGCTCATTA GACTTATTTT AGCCTTGGTA AATGATTGT ACTTGATATC AGTCGTTTC 1809

TTTGAGATAA AATGTTCCCTG TTCAGGAAAT ATAATGTATA TCATAATTAA ACAAAAAA 1869

AAAAA 1874

15

SEQ ID No.:4

Length of Sequence:23

Type of Sequence:Nucleic acid

Strandness:single strand

5

Topology:straight

Kind of Sequence:other nucleic acid synthetic oligonucleotide

ATTGGTGGCG ACGACTCCTG GAG

10

SEQ ID No.:5

Length of Sequence:24

Type of Sequence:Nucleic acid

Strandness:single strand

15

Topology:straight

Kind of Sequence:other nucleic acid synthetic oligonucleotide

CCAGACCAAC TGGTAATGGT AGCG

20

SEQ ID No.:6

Length of Sequence:24

Type of Sequence:Nucleic acid

Strandness:single strand

25

Topology:straight

Kind of Sequence:other nucleic acid synthetic oligonucleotide

GCGGTCTACA AGTCAGGCAG TCAT

SEQ ID No.: 7

Length of Sequence: 31

Type of Sequence: Nucleic acid

5 Strandness: single strand

Topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

CATGCCATT TTCCCAAGGC ATGATCGTAC T

10

SEQ ID No.: 8

Length of Sequence: 20

Type of Sequence: Nucleic acid

Strandness: single strand

15

Topology: straight

kind of Sequence: other nucleic acid synthetic oligonucleotide

GGTGTATG TTGGTGATCC.

20

Sequence Listing 9**SEQ ID No.: 9****Length of Sequence: 27****Type of Sequence: Nucleic acid**5 **Strandness: single strand****Topology: straight****Kind of Sequence: other nucleic acid synthetic oligonucleotide**

CACAGATGGT TAGAGAGGCT TACGCAG

10

Sequence Listing 10**SEQ ID No.: 10****Length of Sequence: 27**15 **Type of Sequence: Nucleic acid****Number of chain: single strand****Topology : straight****kind of Sequence: other nucleic acid synthetic oligonucleotide**

20 TCATCGCAAG ACCGGCAACA GGATTCA